AMENDMENTS TO THE SPECIFICATION

IN THE SPECIFICATION

Amend the paragraph on page 10, line 31 as follows:

Figure 6 shows the alignment of the predicted amino acid sequences of the rat ARBP protein (SEQ ID NO: 4) with the predicted protein encoded by the nucleic acid of the mouse homologue (GenBank NM_018819) (SEQ ID NO: 5) and the predicted protein encoded by the nucleic acid of the human homologue (GenBank NM_016098) (SEQ ID NO: 6) using the CLUSTLAW algorithm.

Amend the paragraph on page 11, line 4 as follows:

Figure 7 shows the homology between SEQ ID No. 3 and the nucleotide sequence of the predicted human homologue (GenBank NM_016098) (SEQ ID NO: 7) using the BLAST algorithm.

Amend the paragraph on page 11, line 8 as follows:

Figure 8 shows the homology between SEQ ID No. 3 and the nucleotide sequence of the predicted mouse homologue (GenBank NM_018819) (SEQ ID NO: 8) using the BLAST algorithm.

Amend the paragraph on page 11, line 12 as follows:

Figure 9 shows the homology between predicted ARBP mouse homologue (GenBank NM_018819) (SEQ ID NO: 9) and the human

homologue (GenBank NM_016098) (SEQ ID NO: 20) using the BLAST algorithm.

Amend the paragraph on page 59, line 12 as follows:

Differential display was performed essentially as described by Liang *et al.* (1992) *Science* 257:967-971. In 20 µl PCR reaction volume was added 2 µl reverse transcription reaction mixture, 1x PCR reaction buffer (50mmol/L KCl, 10mmol/L Tris-HCl pH 8.3, 1.5 mmol/L $MgCl_2$), 2.5 µmol/l oligo dT11N, 0.5 µmol/l 5′ random arbitrary primer, 1.25 mmol/l MgCl2, α-^{32}P-dCTP or α-^{33}S-dCTP and 0.5 µl Taq DNA polymerase (5 U/ml). The PCR cycling parameters were as follows: 94 °C for 30 sec, 40 °C for 90 sec, 72 °C for 40 sec for total 40 cycles followed by 72 °C for 10 min. The 5′ random arbitrary primers used are CAAGCGAGGT(SEQ ID NO: 10), CAGTGAGCTG(SEQ ID NO: 11) and GTCACGGAAG(SEQ ID NO: 12). The amplified cDNAs were then separated on a 6% DNA sequencing gel. A number of amplified cDNAs were found to be differentially expressed, as shown in Figure 3.

Amend the paragraph on page 62, line 27 as follows:

RACE was performed using a Marathon-ReadyTM cDNA kit purchased from CLONTECH with rat brain mRNA, according to the manufacturer's protocol. Two primers were used: AP1 (5′-

CCATCCTAATACGACTCACTATAGGGC3' (SEQ ID NO: 13), which is a universal primer of the Marathon-ReadyTM cDNA kit for the inserted cDNA fragments) and a SEQ ID No. 1 specific primer (5'-AGCCGAGAGTTGGTTTGGGGATTC-3' (SEQ ID NO: 14)). The amplified PCR fragment was cloned into pGEM-3Zf(+) (Promega) and sequenced to obtain the full length cDNA of the fragment. The nucleotide sequence (SEQ ID. No.3) of the cDNA is shown in Figure 5.

Amend the paragraph on page 64, line 6 as follows:

Total RNA was prepared from L4 and L5 DRG ganglia (n = 3) according to the acid guanidinium thiocyanate-phenol-chloroform method (Chomczynski, P. & Sacchi, N. 1987 Single-step method of RNA isolation by acid guanidinium thiocyanate-phenol-chloroform extraction. *Anal. Biochem.*, 162, 156 159.) using an RNA isolation kit (Advanced Biotechnologies, Leatherhead, UK). The RNA was treated with DNase (Promega, USA) to remove possible contaminating genomic DNA and then directly subjected to first-strand cDNA synthesis. PCR primers for amplification of ARBP and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) control were designed corresponding to the coding region of the genes as follows: Primer I (ARBP cDNA 5' primer) 5'GGGATCCAACAGCACGGCCATG-3' (SEQ ID NO: 15) and primer II (ARBP cDNA 3' primer) 5'-GGAATTCATTGATAAGGCAGCCGAGA-3' (SEQ ID NO:

16); GAPDH primers, sense 5'-TGCTGGTGCTGAGTATGTCG-3' (SEQ ID NO: 17) and antisense 5'-GCATGTCAGATCCACAACGG-3' (SEQ ID NO: 18). The housekeeping gene GAPDH was amplified separately and in parallel to serve as an internal control. PCR reactions were performed in a 30 µL volume using Red-hot DNA polymerase (Advanced Biotechnologies) on a Perkin DNA Thermal Cycler (Perkin Elmer, USA). All PCR samples were heated at 95 °C for 2 min and then amplified in cycles with a programmed profile of 95 °C, 30 s; 55 °C, 30 s; 72 °C, 60 s; followed by a final incubation at 72 °C for 10 min after the last cycle. PCR cycle numbers were 33 for NGF and NT3, and 25 for GAPDH, which were within the determined linear range of standard curves for the individuals.

Amend the paragraph on page 65, line 5 as follows:

Fresh dorsal root ganglia, superior cervical ganglia, trigeminal ganglia and olfactory bulb were dissected from adult rats, and homogenized in Tris buffer with a protease inhibitor tablet (Roche) at ration of 1 mg tissue per 10 microlitres of inhibitor. The homogenate was centrifuged and supernatant was used for SDS-PAGE. 10 microlitres of the sample was loaded with loading buffer and separated by electrophoresis. The protein was transferred to nitrocellulose membrane and probed with a polyclonal antibody against a C-terminal 14 amino acid peptide

sequence of ARBP (Gly Arg Leu Ile Asn Tyr Glu Met Ser Lys Arg Pro Ser Ala) (SEQ ID NO: 19), prepared as described in Example 10. The bands were visualized with a chemiluminescent method (Roche) on an X-ray film].

Amend the paragraph on page 68, line 32 as follows:

To construct sense and antisense ARBP expression vectors, the following primers were used to amplify ARBP DNA for cloning: Primer I (ARBP cDNA 5' primer) 5'GGGATCCAACAGCACGGCCATG-3' (SEQ ID NO: 15) and primer II (ARBP cDNA 3' primer) 5'-GGAATTCATTGATAAGGCAGCCGAGA-3' (SEQ ID NO: 16). The primers were used to amplify the coding sequence of ARBP and the PCR products digested with *EcoR*I and *BamH*I and cloned into pGEM-3Zf(+). The ARBP coding sequence from the recombinant pGEM-3Zf(+) plasmid was digested with *EcoR*I, *BamH*I or *EcoR*I/*Xba*I and then cloned into *EcoR*I, *BamH*I and EcoRI/*Xba*I digested pcDNA3.1(+)/Zeo respectively to produce sense and anti-sense ARBP expression vectors.

IN THE SEQUENCE LISTING

Please delete the Sequence Listing as originally filed on pages 71 and 72 of the specification and renumber the remaining pages of the specification accordingly. Please insert the Substitute Sequence Listing enclosed herewith immediately after the abstract.